

HIV1LAI	(DP-178; SEQ ID:1)	YTSLIHSLIEESQNQQEKNEQELLELDKwasLYNNMF
HIV1SF2	(DP-185; SEQ ID:3)	YTNTIYNLLEESQNQQEKNEQELLELDKwasLYNNMF
HIV1RF	(SEQ ID:4)	YTGIIYNLLEESQNQQEKNEQELLELDKwanLYNNMF
HIV1MN	(SEQ ID:5)	YTSIYSLLEKSQTQQEKNEQELLELDKwasLYNNMF
HIV2R0D	(SEQ ID:6)	LEANISKSLEQAQIQQEKNMYLEOKLNShDIFGNMF
HIV2NIHZ	(SEQ ID:7)	LEANISQSLEQAQIQQEKNMYLEOKLNSMDVFTNWl
DP180	(SEQ ID:2)	SSESFTLLEQNNNNKLQLAEQWLEQINEKHYLEDIS
DP118	(SEQ ID:10)	QQLDWVKRQQEMRLTWWGTKNLQARYTAIEKYLKDQ
DP125	(SEQ ID:8)	CGGNINLLRAIAEQQHLLQLTVWGIKQLQARI LAVERYLLKDQ
DP116	(SEQ ID:9)	LQARIL AVERYLLKDQQ

FIG. 1

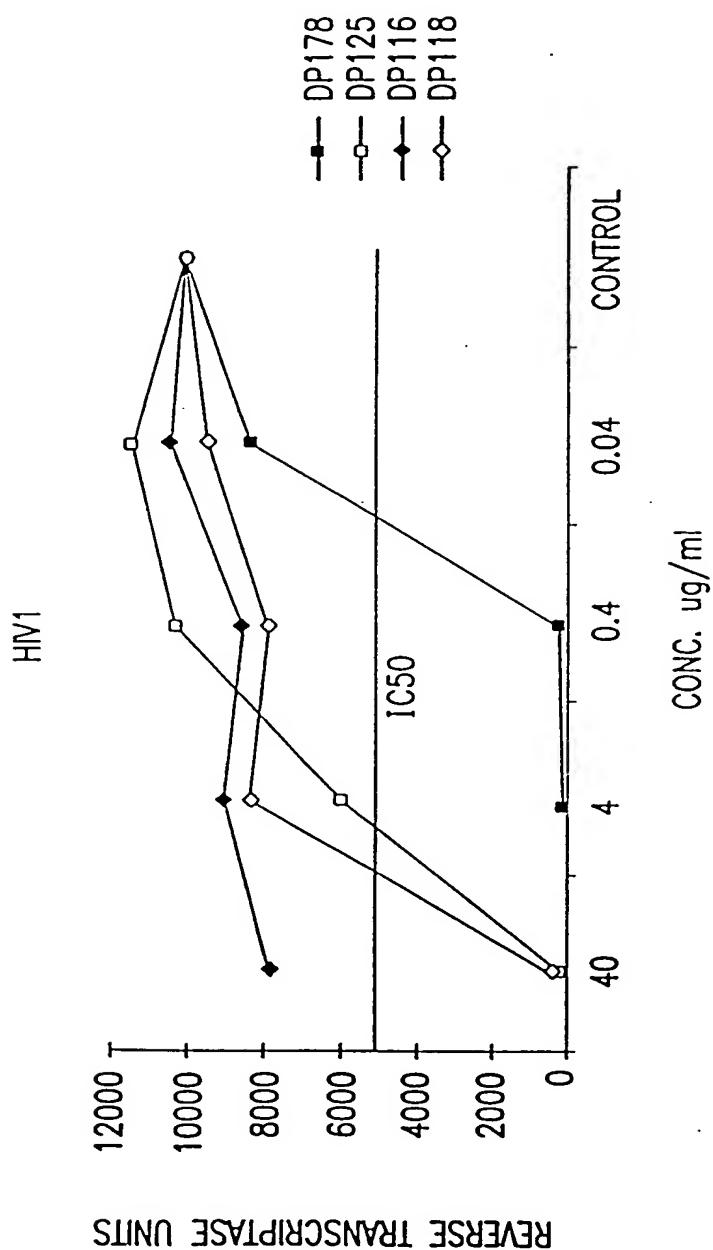


FIG. 2

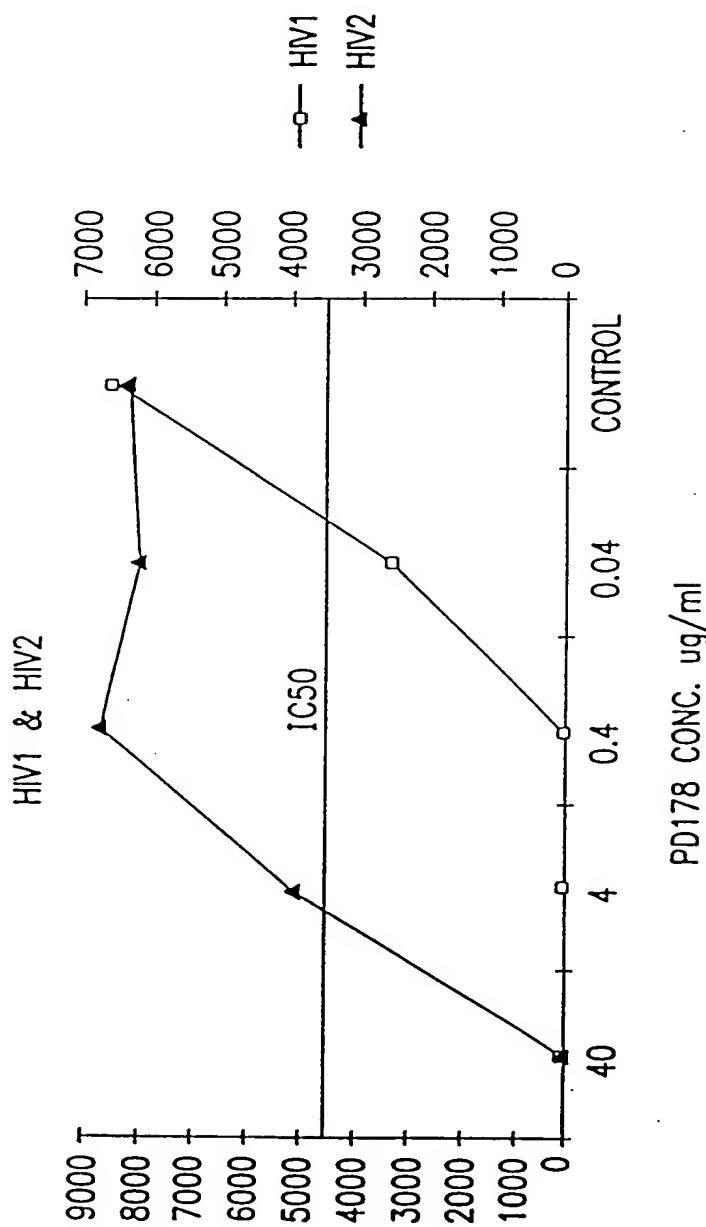


FIG. 3

<u>Number of Syncylio/well: concentration in µg/ml (micrograms/ml)</u>									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncylio</i>									
HIV1LAI	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncylio</i>									
HIV1LAI	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncylio</i>									
HIV1LAI	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncylio</i>									
HIV1LAI	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncylio</i>									
HIV1LAI	0	0	0	0	0	0	0	ND	60

FIG.4B

7872-020 (SHEET 5 OF 63)

<u>HIV1</u>								
Number of Syncyria/well: concentration in ng/ml (nanograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncyria</i>								
HIV1	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncyria</i>								
HIV1	ND	48	ND	ND	ND	ND	ND	ND
<u>HIV2</u>								
Number of Syncyria/well: concentration in μ g/ml (micrograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncyria</i>								
HIV2	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncyria</i>								
HIV2	ND	58	ND	ND	ND	ND	ND	ND

FIG.5

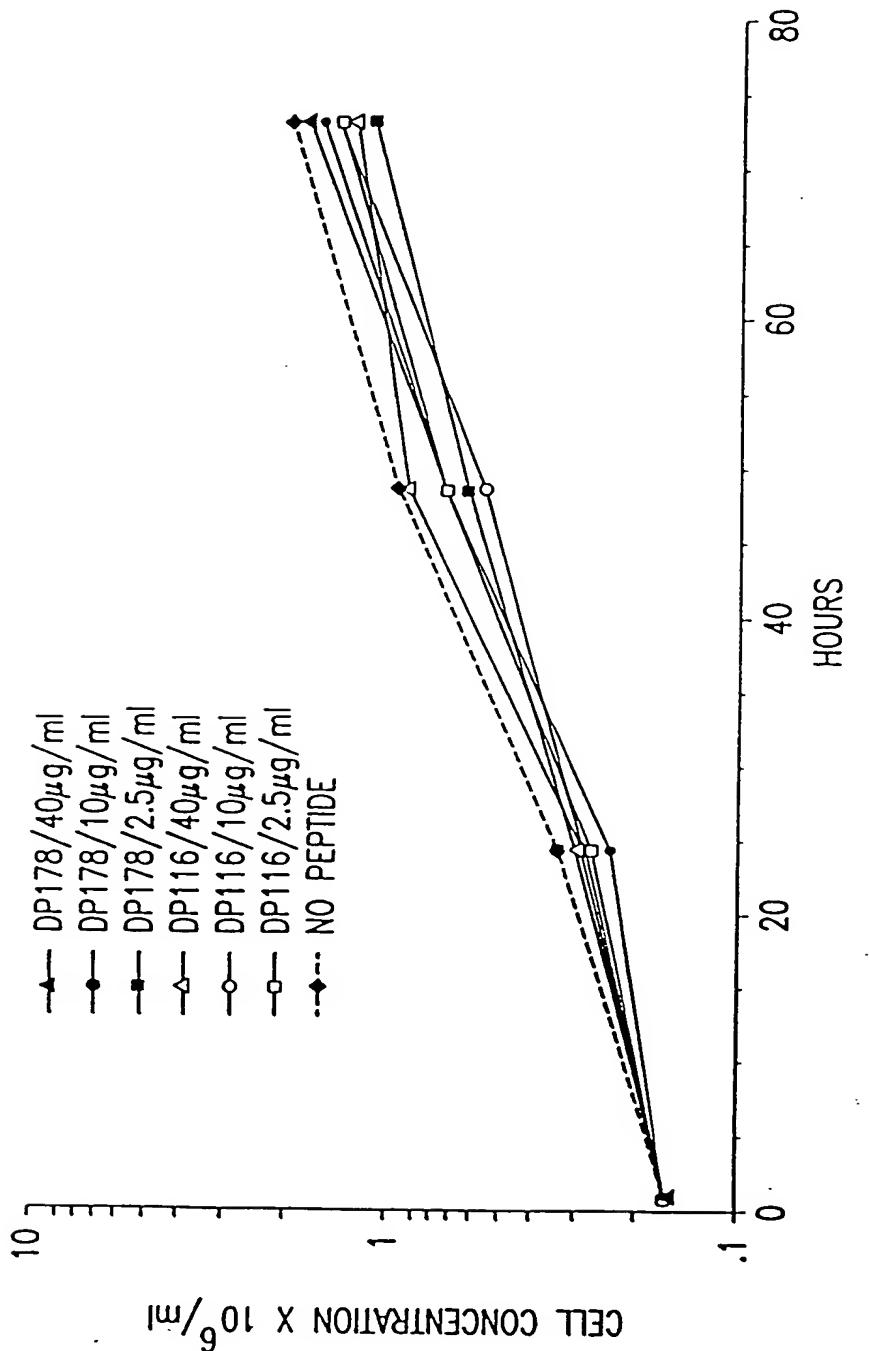


FIG. 6

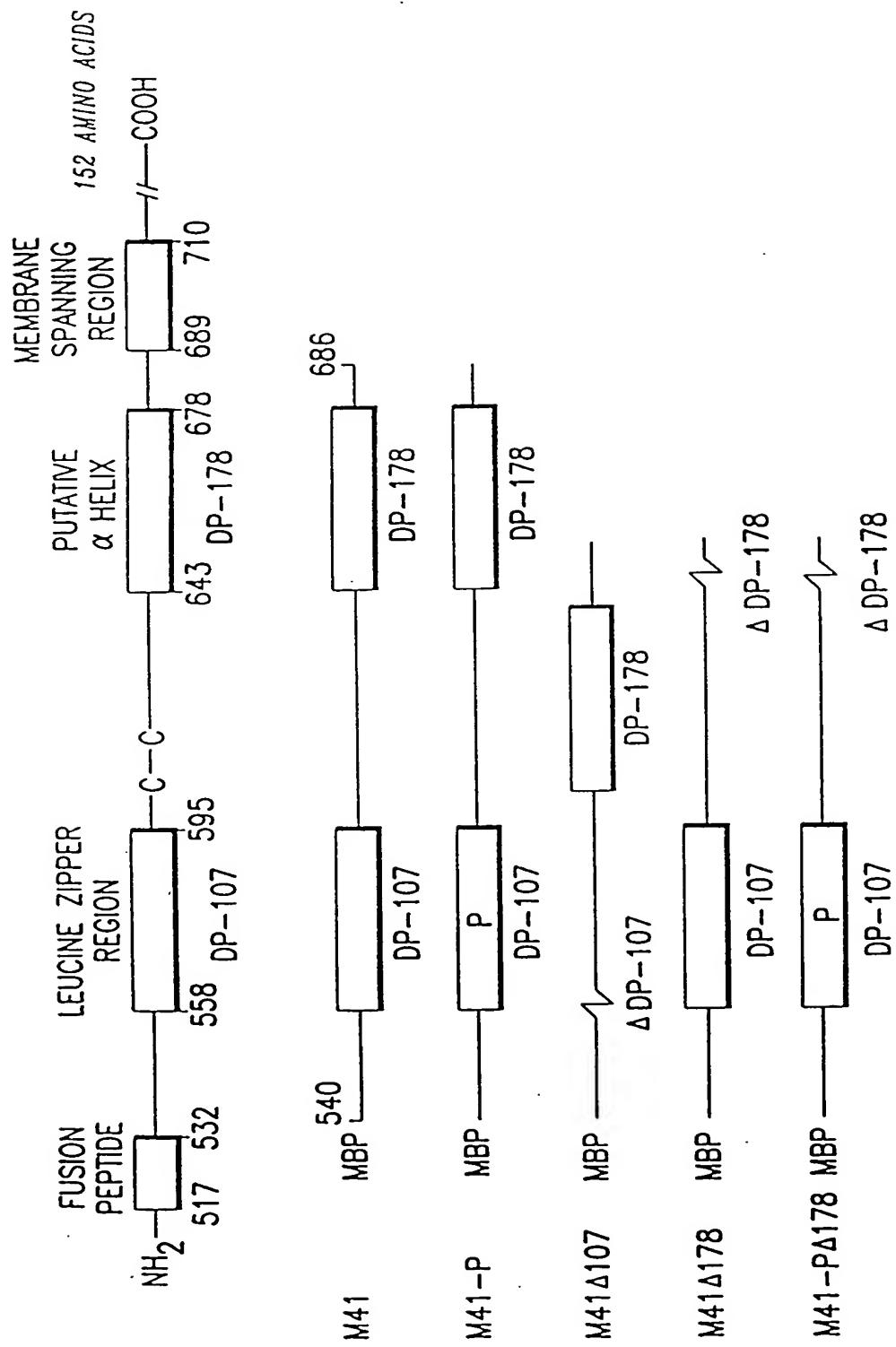


FIG. 7

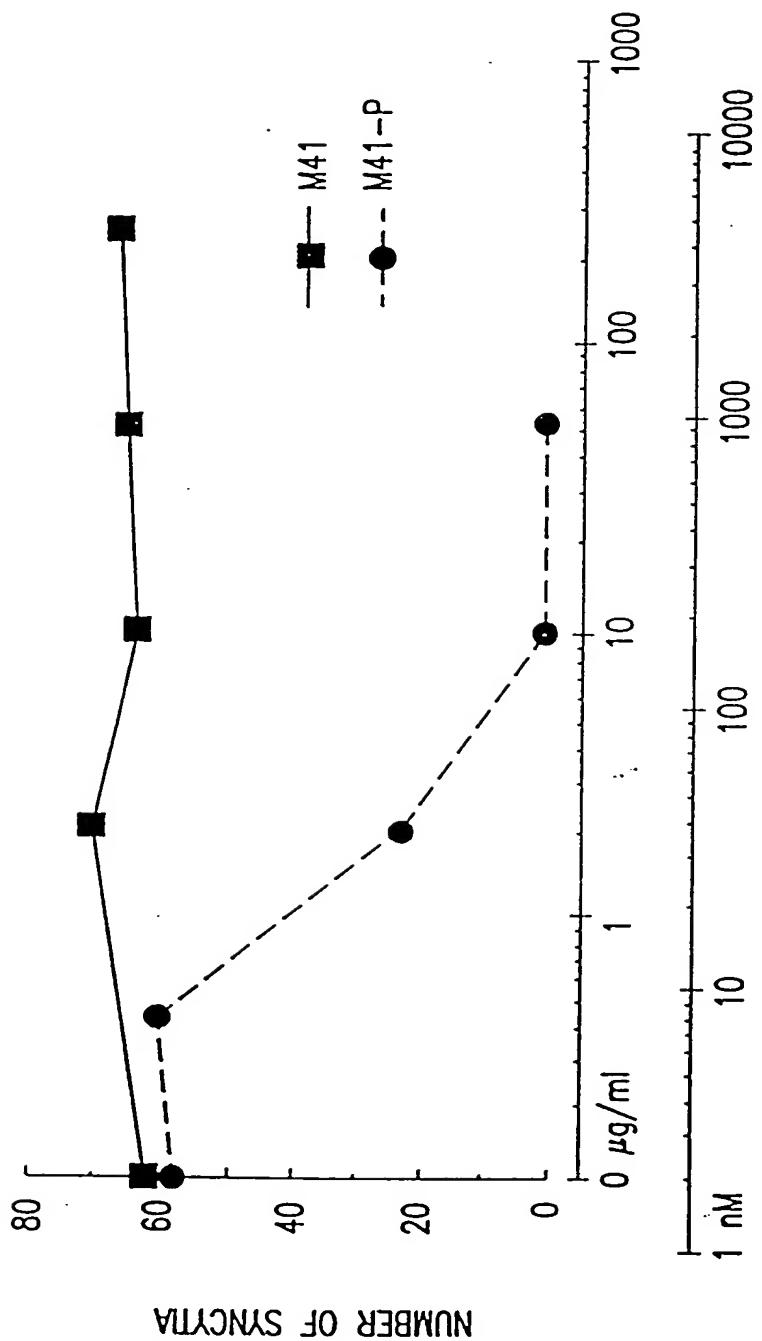


FIG.8

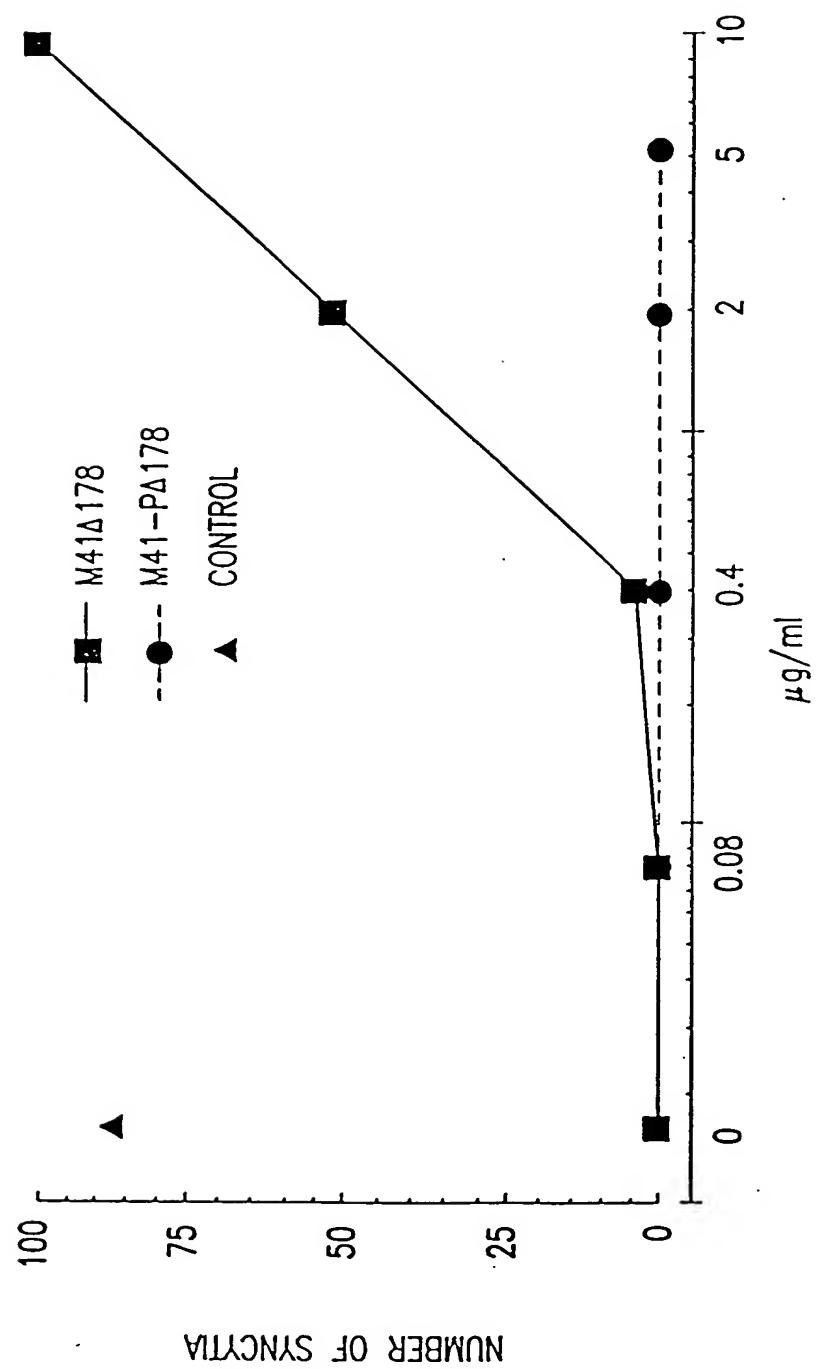


FIG. 9

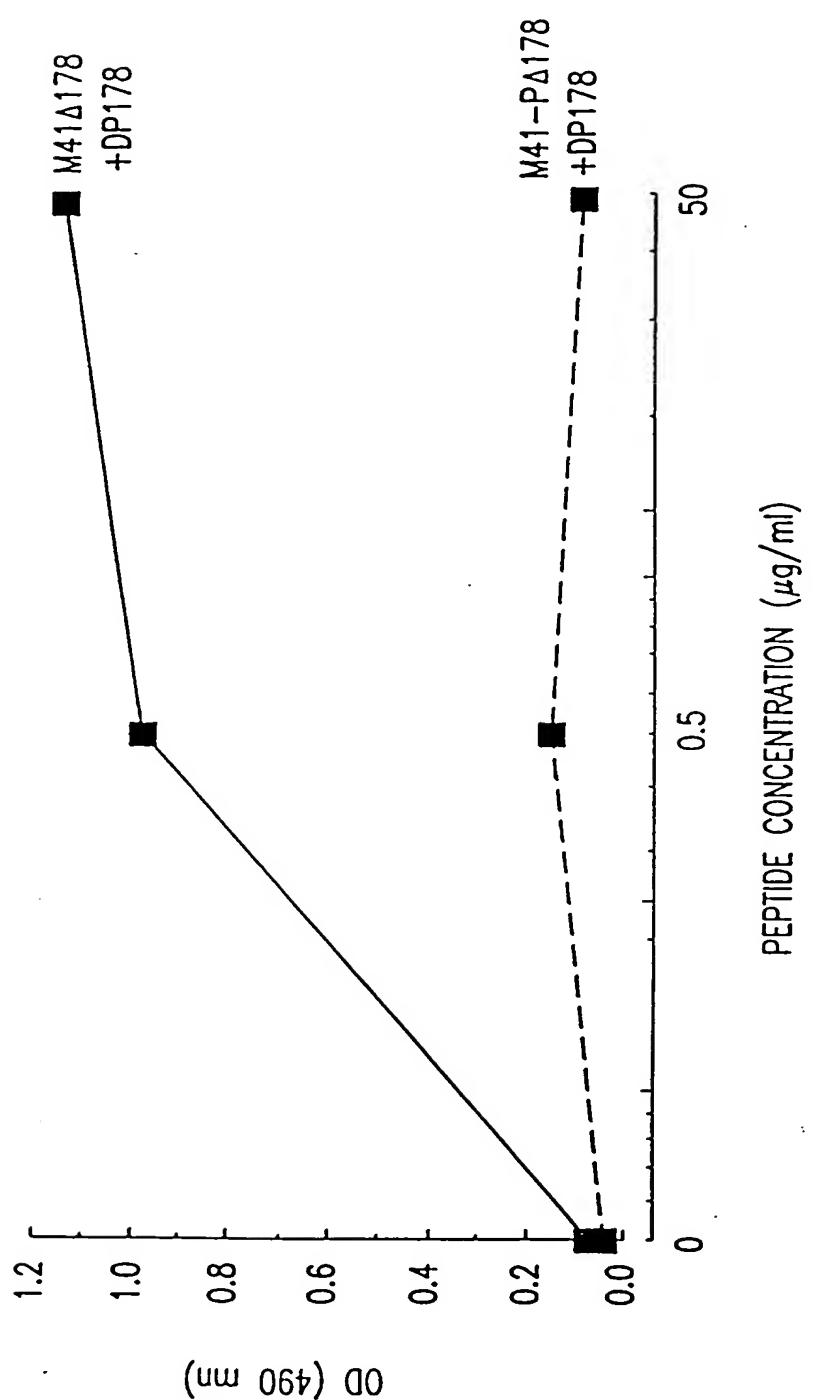


FIG. 10

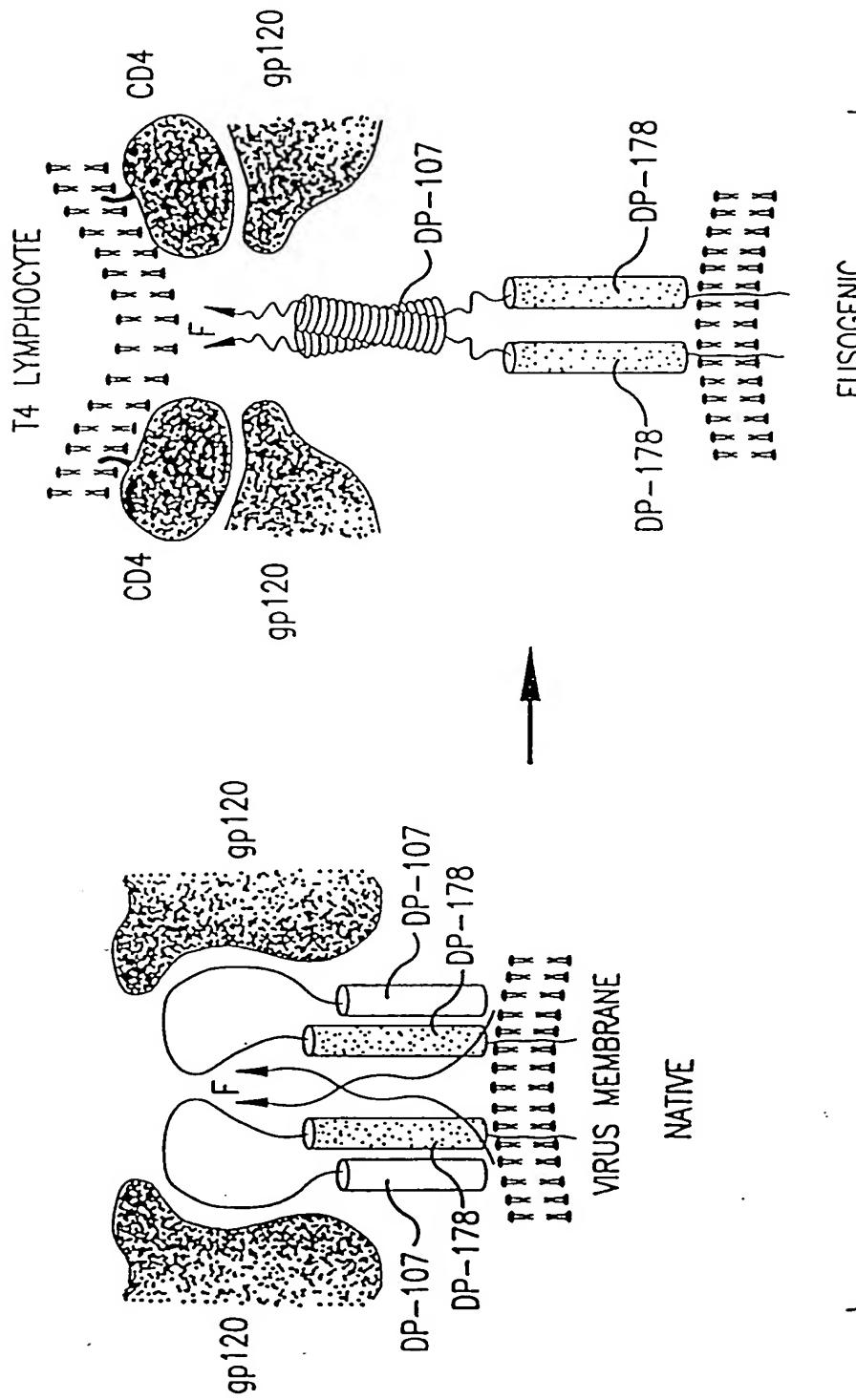


FIG. 11A

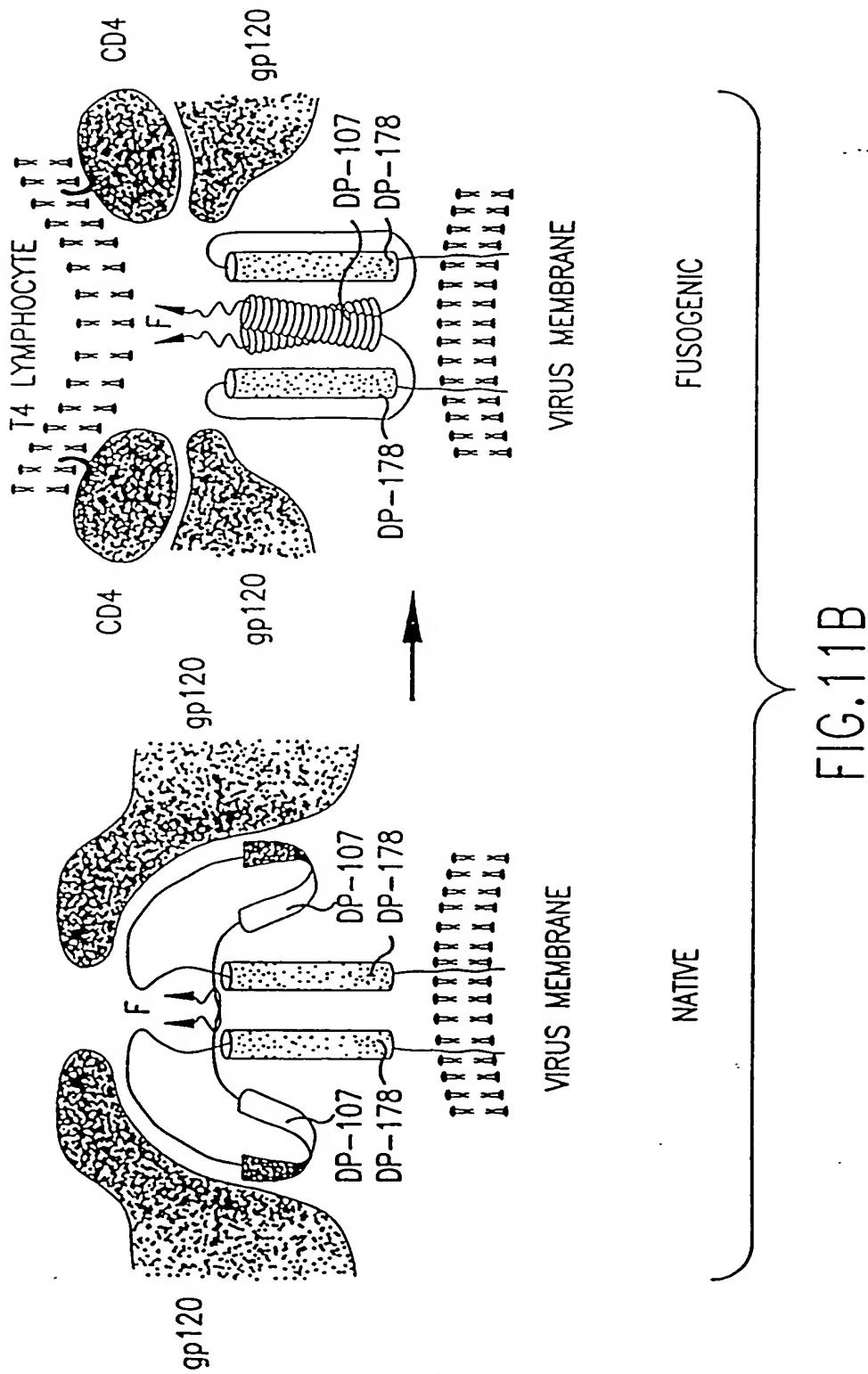


FIG. 11B

Sequence	Positions										Motifs
	D	A	D	A	D	A	D	A	D	A	
GCN4 (gcn4 yeast)	M K Q L E D K V F E L L S K N Y H L E N F V A R L K K L	[L,M,V]	{C,F,G,I,P,T,W}								
C-FOS (fos_human)	T D T L Q A E T D Q L E K S A L Q T E I A N L L K E	[K,L]	{C,F,G,H,I,P,R,W,Y}								
C-JUN (lap1_human)	I A R L E E K V K T L K A Q N S E L A S T A N M L R E Q	[A,I,L,N,V]	{C,D,F,G,H,I,L,P,V,W,Y}								
C-MYC (myo_human)	E Q K L I S E E D O L L E K R R E Q O L K H K L E Q L R N S	[E,L,R]	{A,C,F,G,A,P,W,Y}								
FLU LOOP 36	I E K T N E K F H Q I E K E F S E V E G R I Q D L E K Y	[F,I,L,T,V]	{A,C,F,I,M,P,T,W,Y}								

FIG.12

Sequence	Mol(i)s			
	D	A	D	A
DP-107 (env_hv1bru)Y1=D	[ILOI]	{CFIMPSTY}	[ILQI]	{CFIMPSTY}
DP-107 (env_hv1bru)Y1=D	[ILQIV]	{CDFIMPSTY}	[ILQIV]	{CDFIMPSTY}
DP-107 (env_hv1bru)Y1=D	[ILQIV]	{CDFIMPSTY}	[ILQIV]	{CDFIMPSTY}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{CDFKAPSYY}	[EKLNOV]	{CDFKAPSYY}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{CFGKAPS}	[EKLNOV]	{CFGKAPS}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{CFKAPS}	[EKLNOV]	{CFKAPS}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{ACFGMPRVYY}	[EKLNOV]	{ACFGMPRVYY}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{CFGKAPRY}	[EKLNOV]	{CFGKAPRY}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{EFGKAPRY}	[EKLNOV]	{EFGKAPRY}
DP-107 (env_hv1bru)Y1=D	[EKLNOV]	{ACFGMPRVYY}	[EKLNOV]	{ACFGMPRVYY}
DP-107 (env_hv1bru)Y1=A	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K
DP-107 (env_hv1bru)Y1=A	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-107 (env_hv1bru)Y1=A	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W F	[YTSL]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W F
DP-178 (env_hv1bru)Y1=A	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=A	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=A	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=A	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=D	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=D	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=D	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W
DP-178 (env_hv1bru)Y1=D	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W	[YTSLI]	I H S L I E S Q N Q E K N E Q E L L E L D K W A S L W N W

FIG. 13

Sequence	Positions										Hybrid Motif
GCN4 (gcn4 yeast)	A	D	A	D	A	D	A	D	A	D	0
DP-107 (env_hv1bru)[1=0]	W K Q L	E D K V E E I I L S K N Y H I L E N E V A R I K K L									[LMNV] {CFGIMPWTW}
DP-107 (env_hv1bru)[1=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{ILQT} {CFIMPSTY}
DP-107 (env_hv1bru)[1=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{ILQTV} {CFIMPST}
DP-107 (env_hv1bru)[1=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{ILQTV} {CFIMPST}
DP-107 (env_hv1bru)[1=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{ILQTV} {CFIMPST}
DP-107 (env_hv1bru)[2=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{EKLNAQV} {EKFKAQSY}
DP-107 (env_hv1bru)[2=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{EKLNAQV} {EKFKAQSY}
DP-107 (env_hv1bru)[2=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{EKLNAQV} {EKFKAQSY}
DP-107 (env_hv1bru)[2=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{EKLNAQV} {EKFKAQSY}
DP-107 (env_hv1bru)[2=0]	N N L L R A	I E A Q Q H L L Q L I V W G I K Q L Q A R I									{EKLNAQV} {EKFKAQSY}

FIG. 14

Sequence	Positions										Parent Motif	Hybrid Motif													
	A	D	A	D	A	D	A	D	A	D															
GCA4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	I	S	K	N	Y	H	L	E	N	V	A	R	I	K	L	[LMNV] {CFGIMPW}
DP-178 (env_hv1brv)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	O	Q	E	X	N	E	Q	E	L	L	D	K	[EKLQY] {ACFGAPRWY}
DP-178 (env_hv1brv)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	O	Q	E	K	N	E	O	E	L	L	D	K	[EKLQWY] {ACFGAPRY}
DP-178 (env_hv1brv)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EKLQMY] {ACFGAPRY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPRWY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPRY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPWY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPWY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPWY}
DP-178 (env_hv1brv)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	Q	E	K	N	E	Q	E	L	L	D	K	[EILNQSY] {ACFGAPWY}

FIG. 15

Sequence	Positions												Parent Motif	Hybrid Motif
	A	D	A	D	A	D	A	D	A	D	A	D		
DP-107 (env_hvibr) Y1=0	N	N	L	R	A	I	E	A	Q	O	H	L	Q	[ILQIV] {CQFIMPST}
DP-107 (env_hvibr) Y1=0	N	N	L	R	A	I	E	A	Q	O	H	L	Q	[EXLNQV] {CFKAPS}
DP-178 (env_hvibr) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	[EFKQWY] {CGGPRVY}
DP-178 (env_hvibr) Y1=0	Y	T	S	L	I	H	S	L	I	E	S	Q	N	[EFILNQSYM] {CFGPRVY}
FLU loop 36	I	E	K	I	N	E	K	F	H	Q	I	E	F	[FLIV] {ACFLQPTVWY}

FIG. 16

FIG. 17

Sequence	Positions				Parent Motif	Hybrid Motif
	A	D	A	D		
GCN4 (gcn4 yeast)	W K Q L E D K Y V E F I L S K N Y H L E N E V A R I K K L				[LMAV] {CCGIMPW}	
DP-107 (env_hv1brv)Y1=D	N N L L R A I E A Q H L L Q L I V W G I K Q L Q A R I L A V E R Y L K D Q				[ILQTY] {CDFIMPSI}	
DP-107 (env_hv1brv)Y2=D	N N L L R A I E A Q O H L L Q L I V W G I K Q L Q A R I L A V E R Y L K D Q				[EKLNQY] {CFKRPQS}	
DP-178 (env_hv1brv)Y1=A	Y T S L I H S L I E S Q N O Q E K N E Q E L L E L D K W A S L W N W F				[EFKLQMY] {CFGAPRYV}	
DP-178 (env_hv1brv)Y1=D	Y T S L I H S L I E S Q N O Q E K N E Q E L L E L D K W A S L W N W F				[EFLNQSY] {CCGAPRVY}	
C-FOS (fos_human)	I D I L Q A E I D Q L E D E K S A L O T E I A N L L K E				[IKL] {CGHILPRWY}	
C-JUN (fop1_human)	I A R L E E K V K T I L K A Q N S E L A S T A N W L R E Q				[AILNV] {CDFGHILPWWM}	
C-MYC (myo_human)	E Q K L I S E E D L L E K R R E Q L K H K L E Q L R N S				[ELR] {ACFGMPWY}	
FLU LOOP 36	I E K T N E K F H Q I E K E F S E V E G R I Q D L E K Y				[FILTIV] {ACELKPWIK}	
					[AEFIKLMAORSTWYX]	{CFP}
					=	{CDGHP} {CFP}

FIG. 18

P-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
P-[P](1)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](2)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](3)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](4)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](5)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](6)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](7)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](8)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](9)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-[P](10)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-X(1,12)-[LIV]-P(6)-[LIV]-P(6)-[LIV]
P-X(13,23)-[LIV]-P(6)-[LIV]-P(6)-[LIV]

FIG. 19

Fusion ♦ ALLMOT15 ♦
Peptide ♦ 107x178x4 ♦
♦FLGFLG A AGSTMGARSM TLTQARQ ♦ LL SGIVQQQ DP107-NNL

LRAIEAQOHL LOLTVWGIKO LOARILAVER YLKDO-DP107 QLLG♦♦ I WGC

♦ 107x178x4 ♦
♦ ALLMOT15 ♦ *LVS Coiled-Coil*
SGKLICT TAVP ♦ WNASWS NKSLEQIWNN MTWM *E ♦ WDREIINN DP178-

YTSLIHSL IEESONOQEK NEOELLELDK* RASLWNWT-DP178 NI

♦ Transmembrane Region ♦
TNWLVYIK♦♦ DTMIVGGGLVGLRIVFAVLSIV NRVRQGYS♦ PL

♦ P23LZIPC ♦
SFQTHLPTPR GPDR ♦ PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL ♦ CL

♦ ALLMOT15 ♦ ♦ 107x178x4 ♦
F ♦ SYHRLRDLL LIVTRIVELL GRRGW ♦ EALKY WWNLLOXWSQ

ELKNSAVSLL NAT♦ AIAVAEG TDRVIEVVQG A♦ CRAIRHPR

RIRQGLERIL L

FIG. 20

Fusion	▼ALLMOT15▼
Peptide	▲107x178x4▲
▼.....ELGEL	LGVGSALAS GVA ▲ <u>VSKVLHL EGEVNKIKSA</u>

+P1&12LZIPC+
LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ ▲▼ LL +PIVNKQ
 ^107x178x4^
 SC ▲SISNIETYI + EQQQKNNRLLEITREEFVNAG + VTIPVSTMLTINSELLSL

+P1&12LZIPC+
 ▼ALLMOT15▼
 INDM +PI ▼TNDQ KKLMNSNNVQI V+ RQQSYSI+ MS IIKEEVLAYV
 VQ▼ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLRTDRG WYCDNAGSVS
 FFPQAETCKV QSNRVFCDTM NSLTPSEIN LCNVDIFNPK
 YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG
 IIKTFSGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7, 12, & 23LZIPC+
 ▲107x178x4▲ ▼ALLMOT15▼
 EPIINFYDPLVF +PSDE ▲FDASISQVNEKINQSLAF ▼I+ RKSDELL+

♦Transmembrane Region♦
 HNVNA+ GK STTN ♦IMTTIIVIVIVILLSLIAVGLLLY+ C+
 KARSTPVTLS KDQLSGINNI AFSN

Fusion Peptide ELGELG **▼ALLMOTIS▼ ^{▲107x178x4▲} ▼AAGTA MGAAA [▲]TALTYQSQHILLAGILQQQIQNLLAAY**

EAQ▲ QQM ^{▲107x178x4▲} LKLTIWGVIKNLNARVTALEKYLEDQARLN▲ AWG▼ CA

LVS Coiled-Coil
▼ALLMOTIS▼ ^{▲107x178x4▲} WKQVCHTTVP WQWNNRTPDW ▼NNMT *WLE [▲]WERQISYLEGNTT

TOLEEARAOEEKNLD▲ AYQKLSS* WSDFWSW▼ FDF ^{▲107x178x4▲} SKWLN ▲ILK

**♦ Transmembrane Region ♦
IGELDYLGNGLRLLYTV▲ XS▲ CIARVRQGYS PLSPQIHIHP WKGQPDNAEG**

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS FWLYNS

**▼ALLMOTIS▼
▼CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL▼**

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22

Fusion *107x178x4*
 Peptide *LVS Coiled-Coil*
EAG *SNLNAQAIQ

SLRTSLEOSNKAIIEEIREATOETVIA* VOGYODY* VNNEL \blacktriangledown VP
ALLMOTIS
107x178x4
+P6 & 12LZIPC+
 AMQHMSCELVGQRLGLRLLRYYTTELLSIFGPSLRD +PISA + EISIQALIYAL

GGEIIHKILEKLGYSGSD* MIAILESRGIKTKI \blacktriangledown THVDLPGKF IILSISY
+P1 & 12LZIPC+
+PTLSEVKGVIVHRLEAV+ SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSQNSL YPMSPPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA
 NCASILCKCY STSTINQSP DKLLTFLASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil
 ALLMOTIS
 +P12 & 23LZIPC+
 DMVYEGKVAL G *PAISLD *VRL*DVGTNLGNALKLDDAKVLI+

* Transmembrane Region *
 DSS+ NQILETYRRS \blacktriangledown SFN *FGSLL SVPILSCTAL ALLLLIXCC*
 K RRYQQTLKQH TKVDPAFKPD LTGTTSKSYVR SL

Fusion **▼ALLMOTIS▼**
Peptide **▲107x178x4▲**
▼.....ELGAI IGSVALGVA TAAQITAASA LIQANQNAAN ▲ILRLKESITA

TIEAVIIEVTDGLSQLAVA▲ VG KM▼ QQFVNDQFNNTAQELDCIKITQQV

▼ALLMOTIS▼
GVELNLYLTELTTV FGPQITSPAL ▲TQLTIQALYNAGGNMDYLLTKLGVG

▲P1 & 12LZIPC▲
NNQLSSLIGSGLIT GN▼ ▲PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTRI VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV LANCKMTTCR CADPPGHSQ

▼ALLMOTIS▼
▲107x178x4▲
NYGEAVSLID RHSCN ▲▼VSLSD GITRLSGEF DATYQKNISI LDSQVVTG

LVS Coiled-Coil
***NLDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTS A ▲Trans-
LIT* XIA**

membrane Region▲
LTAJSLVCGII SLV▼▲ LACYLMY▲ KQKAQQKTLLWLGNNTLGQMRATTKM

FIG. 24

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Fusion **▼ALLMOTIS▼**
Peptide ***107x178x4*** ***LVS Coiled-Coil***
.....EFGGV ***IG ▼TIALG *VATSAQITAVALVEAKQARS DIEKLKE**

AIRDTNKAQOSVQSSIGNLIVAIKSVQ* **DYVNKE▼*** IVPSIARLGCEAAG

▼ALLMOTIS▼
107x178x4
LQLGLALTQH ***▼YSELTNIFGDNIGSLOEKGIKLOGIASLYRTNITE▼***

+P5 & 12LZIPC+
IFTITSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL **+PLLTRLLNTQIYR**

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKITHKECNTIGINGMLFNTNKEGTLAFYTP

▼ALLMOTIS▼
107x178x4
+P6 & 23LZIPC+
NDITLNNSVALD ***PIDI *SIELN ▼KAKSDLEESKEWI* RRSNOKL***

♦Transmembrane Region♦
DSIGNWHOSSTT ***III*** LIM III IFIINVT II* **IIAVKYY▼ R**
IQKRNRRVDQN DKPYVLTNK

FIG. 25

Fusion
Peptide
.....GLEGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

107x178x4

▼ ALLMOTIS ▼
LVS Coiled-Coil
*Q ▼AADLKST ▪ QAAIMQINGKLNRVIEKTNEKTHQIEKEESEVEGRIQ
DLEKYVEDTKIDL* WSYNAELLYALENQHTI ▪ DLT▼ DSEMNLKFKEKTR
RQLRENAEEMGNGCFKTYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG
VELKSGYKDWLWISFAISCFLLCVVLLGFIMWACQRGNIRCNCI

FIG. 26

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			Fusion Army
			Purified (x r T)
			[C60] (ug/ml)
RSV F2	Y TSV	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	RSV F2 AV
T-141	Y TSV	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-142 ++ 39 CO
T-142	Y TSV	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-143 ++ 31
T-143	S V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-144 ++ 114
T-144	S V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-145 ++ 40
T-145	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-146 ++ 281
T-146	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-147 ++ 204
T-147	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-148 ++ 354
T-148	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-149 ++ 336
T-149	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-150 ++ 342
T-150	V I T	T IEL SNI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-151 ++ 116
T-151	S NI	S NI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-152 ++ 117
T-152	S NI	S NI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-153 ++ 280
T-153	S NI	S NI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-154 ++ 118
T-154	S NI	S NI KEN K C N G A K V K L I K O E L D K Y K N A V T E L Q Q L M Q S T	T-155 ++ 253
T-155			

FIG. 27A

RSV	Peplole #	AVG. IC50 (XTT) ug/ml
T-22	I E L S N I K E N K C N G T D A K Y K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-23	I E L S N I K E N K C N G T D A K Y K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-24	E N K C N G T D A K Y K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-25	D A K V K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-26	C N G T D A K V K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-27	S N I K E N K C N G T D A K V K L I K Q E L D O K Y K N A V T E L Q L L M Q S T	>500
T-68	V S K Q Y S A L R T Q W Y T S V I T I E L S N I K E N	165
T-334	A F I R K S D E L L H N V	26
T-371	Y T 8 V I T I E L S N I K E N K U N O D A K V K L I K Q E L D O K Y K N	>500
T-372	T 9 V I T I E L S N I K E N K U N O D A K V K L I K Q E L D O K Y K N	NOT TESTED
T-373	S V I T I E L S N I K E N K U N O D A K V K L I K Q E L D O K Y K N A	>500
T-374	8 N I K E N K U N O D A K V K L I K Q E L D O K Y K N A V T E L L O L L M Q S T	>500
T-375	K E N K U N O D A K V K L I K Q E L D O K Y K N A V T E L L O L L M Q S T	>500
T-376	A V S K Q Y L S A L R T Q W Y T S V I T I E L S N I K E N K U N O I D A	>100

F I 6 . 2 7 B

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RSV DP-I07-LIKE REGION (F1)		Function Assay	Primed (norm)	(S10 X 777)
RSV			84V	
T-107	A S Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-107	AV	
T-110	A S Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-110	-	204
T-121	A S Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-121	-	154
T-122	G Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-122	-	347
T-123	G Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-123	-	166
T-124	G Q V A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-124	+	95
T-125	A Y S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-125	+	84
T-126	V S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-126	+	82
T-127	V S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-127	+	89
T-128	V S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-128	+	206
T-129	V S K V L H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-129	+	345
T-130	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-130	-	177
T-131	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-131	-	118
T-132	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-132	-	272
T-133	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-133	-	46
T-134	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-134	-	187
T-135	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-135	+	60
T-136	H L E Q E V N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-136	-	194
T-137	N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-137	-	93
T-138	N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-138	+	38
T-139	N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-139	+	86
T-140	N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-140	+	160
T-141	N K I - A L L S T I N K A V V S S N A V S U L T B K V L D L K N Y D K O L L	T-141	+	204

F1 G. 27 C

RSV	Peptide #	AVG. IC50 (XTT) ug/ml
T-12	V V S L S N G V S V L T S K V L D L K N Y I D K Q L L	>500
T-13	V V S L S N G V S V L T S K V L D L K N Y I D K Q L L	>500
T-15	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q	>500
T-19	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q	>500
T-28	A S Q V A V S K V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q	>500
T-29	S Q V A V S K V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q	>500
T-30	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q	327
T-69	V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	328
T-70	V N K I K S A L L S T N K A V V S L S N Q V S V L T S K	292
T-66	N D Q K K L M S N N V Q I V R Q Q S Y S I M S I I K E E	349
T-57	S I S N I E T V I E F Q Q K N N R L L E I T R E F S V N A Q V I P V S	>500
		>100

FIG. 27 D

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FIG. 28A

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RSV Peptide #	AVG. IC50 (XTT) ug/ml
T-71 P I I N F Y O P L I V F P S D E F D A S I S Q V N E K I N O S L A F I R	138
T-394 R M K O L E D K V E E L L S K L A F I R K S D E L L H N V	NOT TESTED
T-813 D E L L H N V N A Q K S I	>100
T-614 K S D E L L H N V N A Q K S I	>100
T-815 I R K S D E L L H N V N A Q K S I	>100
T-616 A F I R K S D E L L H N V N A Q K S I	>100
T-617 F D A S I S Q V N E K I N O S L A F I	NOT TESTED
T-692 S L A F I R K S D E L L H N V N A Q K S I	>100
T-683 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	NOT TESTED
T-685 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	7
T-686 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	4
T-687 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	4
T-688 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	5
T-689 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	80
T-670 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	>100
T-671 A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	8
T-672 I S O V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	6
T-673 I Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	14
T-674 I N E K I N O S L A F I R K S D E L L H N V N A Q K S I	>100
T-675 I K I N O S L A F I R K S D E L L H N V N A Q K S I	>100
T-676 I N Q S L A F I R K S D E L L H N V N A Q K S I	>100
T-730 F D A S I S Q V N E K I N O S L A F I R K S D E L L H N V N A Q K S I	NOT TESTED

F I 6. 2 8 3

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HPV3 DP07-LIKE REGION (F1)			[C16] (μ M)	[P(N10)]	AV
157	RPLKEAI RDTNKAQVYQSVQSSIONLIVAIKSVQDYNKEIVP	157	574.	•	•
158	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	158	146.	•	•
159	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	159	207.	•	•
160	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	160	516.	•	•
161	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	161	190.	•	•
162	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	162	401.	•	•
163	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	163	121.	•	•
164	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	164	512.067.	•	•
165	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	165	342.	•	•
166	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	166	310.	•	•
167	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	167	215.	•	•
168	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	168	610.	•	•
169	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	169	137.	•	•
170	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	170	456.	•	•
171	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	171	417.	•	•
172	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	172	61.	•	•
173	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	173	30.	•	•
174	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	174	295.	•	•
175	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	175	312.	•	•
176	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	176	329.	•	•
177	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	177	707.	•	•
178	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	178	218.50.	•	•
179	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	179	67.8	•	•
180	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	180	547.	•	•
181	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	181	613.	•	•
182	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	182	152.	•	•
183	QVATSAQITAAVALVEAKOQARSIDIEKLKEAI RDTNKA	183	669.	•	•

FIG. 29A

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HPV-3 DP07-Like Walks		Avg. (IC50)
T-42	A T S A O I T A A V A L V E A K Q A R S D I E K L K E A	641,000 up/m ²
T-43	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A	653,000 up/m ²
T-39	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V A S V A Q S S	712,000 up/m ²
T-38	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V A S V A Q S S	700,000 up/m ²
T-40	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V A S V A Q S S I O N L I V A	58,708 up/m ²
T-44	A E K L K E A I R D T N K A V A S V A Q S S I O N L I V A	225,140 up/m ²
T-45	I A R D T N K A V A Q B V Q B I O N L I V A I K B V Q D Y V N K E I V	483,000 up/m ²
T-46	A V A S V A Q S S I O N L I V A I K B V Q D Y V N K E I V	846,000 up/m ²
		137,684 up/m ²
T-582 (walked 184)		
		L K E A I R D T N K A V A S V A Q S S I O N L I V A I K S

Fig. 30A

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Fig. 30 B

7872-020 (SHEET 38 OF 63)

Fusion PeptideRNKRGVFVLGFLGFLATAGSAMGAAS ♥ ALLMOTI5 ♥
Peptide ♣ 107x178x4 ♣ ♥ XXXXAQSRTLLAGIVQQQQQ

LLDVVKRQOEELLRLTVWGTKNLOTRVTAIEKYLKDQAQLNAWG CAF

♥ ALLMOTIS ♥
*LVS Predicted Coiled -Coil
RQVCHTTVPWPNASLTPDW *NND ♥ TWQEWERKVDFLEENITALLEEAQIQQ

IYTVMIAKLROGYRPVESSPPSYFOXTHTOOPALPTREGKEGDGGEGGGNNSWP

WOIEYIHF

FIG. 31

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSHGDLFRFSSD

▲107x178x4▲

IQCPSFGTRENHTEGLLMVFKDNIIPYSF ▲KVRSYTKIVTNILYNGWYADSVTNRHE▲

EKFSDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNTVNLKP TGGLANGVRR

YASQTELTYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGGLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTVP VPPTAPGKSL GTLNKPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAALKLG DVISVSQCVN VNQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

▲107x178x4▲

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ▲SLIENIDFASLELYSRDEQRASNVD *LE▲

LVS Predicted Coiled Coil

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

◆P12LZIPC◆

TM Potential

TM Potential

LVSTVGGLFSSLVSGFISFK N ▲PFGGMLILVLVAGVVILVISL◆ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

FIG. 32

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MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ ▲107x178x4▲ +Dimerization+
@KRY KNRVASRKCRAK ▲FK@ Q +LLOIHYREVAAKSSENDRLRLLLKQ▲

MCPSLDVD+ SI IPRTPDVLHE DLLNF

FIG. 33

7872-020 (SHEET 41 OF 63)

Fusion			
Peptide	♥ ALLMOT15 ♥		* <u>LVS Coiled-Coil*</u>
FAG	♥ VVLAGAALGVATAAQITAGIALHQSMIL *NSQAIIDLNRASLETTN		

QAIIEAIIQAGQEMI*LA VQGVQDYINN♥ ELIPS MNQLSCDLIGQKLGLKLLRYYT

÷ P23LZIPC ÷
÷ P6,12LZIPC ÷
▲ 107x178x4 ▲
▼ ALLMOTIS
÷ PISA ▲ ▼ ÉISJOALS

EILSLFGPSLRD ÷ PISA ♡ ÉISIQALSYALGGDINKV ÷ LEKLGYSGGDL ÷

LGILES♦ RGKARI♥ THVDTESYFIVLSIAY ♦PTLSEIKGVTVHRLEGV♦ SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

÷P23LZIPC÷
÷P12LZIPC÷
♥ALLMOT15♥
LVS Coiled-Coil
DHCPVVEVNGVTIOVGSRRYPDAVYLHRIDLGP ÷P ♥IS*LERLDVGTNLGN

◆ Transmembrane Region ◆
AIAKLEDAKELL+ ESSDOI*L+ RSMK ◆ GLSSTSIVYILI♥ AVCLGGLIGIP

ALICCC♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL.

FIG. 34

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Pre S1 and Pre S2

MGQNLSTS~~NPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG~~
LGFTPPHGGLLGWSPQAQGILQTL PANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQLDPRVRGLYFPAGGSSGTVNVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

♦P12 & 23LZIPC♦

MENITSG FLG ♦PLL VLQAGFLLTRILTI♦ PQSLDSWWTSLNFLGGTTVCLG

♦P12 & 23LZIPC♦

QNSQSPTSNHSPTSCPPTC ♦PGYRWMCRRFIIFLFILLCLIFLLVLLDYQGML♦
PVCPLIPGSSTTSTGPCRTCM~~TAQGTSMYPSCCCTKPSDGNC~~TCIPIPSSWAFGKF

♦Transmembrane Region♦

LWEWASARFSWLS ♦LLVPFVQWFVGLSPTVWLSVI♦ WMMWYWGPSL

♦Transmembrane Region♦

♦YSILSPFLPLLPIFFCLWVYI♦

FIG. 35

Fusion Peptide **▼ALLMOT15▼** **▲107x178x4▲**
***LVS Coiled Coil**
 AIQLIPLFVG LGI **▼TTAVSTGAAGLGVS** **▲IT *QYTKLSHQQLISDV**

QAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE▲ QGGI▼

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRQLIDNPFWTSFHG

FLPYVMPPLLGPLLCLLLVL¹SFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....????????????????????????????.....

FIG 36

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MKAQKGFTLI ELMIVVVAIIG ILAAIAIPQ

♦ 107x178x4 ♦

♥ ALLMOTIS ♥

♦ ♥ YQDYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA ♦ T ♥

PK DTQYDIGFT

♦ 107x178x4 ♦

♥ ALLMOTIS ♥

♦ ♥ ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS ♦ AIKGAVITVSR ♥

KNDGV WNCKITKPT AWKPNYAPAN CPKS

FIG. 37

7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

▲107x178x4▲

▼ALLMOTIS▼

▲▼KDNTSAGVASSSIKGKYVKEVKVENGVVTAT▲

MNSSNVNKEIQGKKLSLWAKRQDGSVKW▼

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38

7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

♦ 107x178x4 ♦
♥ ALLMOTIS ♥
♦ ♥ SWKNVDKENNFTLKNEQTTADYATNVNI ♥

QLMESNGTKAISVVGKETE ♥

DF MHTNNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

FIG. 39

MNKKLLMNFF IVSPLLATT ATDFTPVP

▲107x178x4▲

♥ALLMOTI5♥

▲♥LSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS▲♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

▲107x178x4▲

▲DLNTKRTKKSQHTSEGTYIHFOJSGVT▲

N TEKLPTPIEL PLKVVKVHGKD SPLKYG

♦P12LZIPC♦

♦PKFDKKQLAISTLDFEIRHQLTQI♦

HGLYRSSDKT GGYWKITMND GSTYQSDL SK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40

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▼ ALLMOTIS ▼
MKKTAFILLL FIALTLLTSP L ▼ VNG

▲ 107x178x4 ▲
LVS Predicted Coiled-Coil
S ▲ EKSEEINEKDLRKKSELQRNALSNLRQIY YYNEKAITENKESDD▲

QFLENTLL ▼ FKG FFTGHPW

▲ 107x178x4 ▲
▲ YNDLLVDLGSKDATNKYKGKKV р DLYGAY ▲

YGYQCAGGTPNKTACMYGGVTLDN NRLTEEKKVP INLWIDGKQTTV

♦ P12LZIPC ♦
♦ PIDKVKT SKKEVTVQELDL ♦ QARHYLHGK FGLYNSDSF GGK VQ

♦ P12LZIPC ♦
RGLIVF HSSEGSTVSY DLFDAQGQY ♦ P DTLLRIYRDН KTINSENЛHI ♦

DLYLYTT

FIG. 41

7872-020 (SHEET 49 OF 63)

MKKTAFTLLL FIALTLLTSP L
♦ ALLMOTIS ♦
♦ VNGS

▲ 107x178x4 ♠
♦ EKSEEINEKDLRKKS ELOQTA LGNL KQDYY YNEAKTENKESHD ♠ Q ♠

FLQHTILFKG FFTDH SWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

▲ 107x178x4 ♠
♦ ALLMOTIS ♦
♦ P12LZIPC ♦
♦ P ♦ L ♠ ETVKTNKKNVTVQELDLQARRYL ♦ QEKYNNLYN ♠

SDVFDGKVQR ♦ GLIVF HTSTE

♦ P23LZIPC ♦
♦ PSVNYDLFGAQGQYSNTLLRIYRDNKTI NSEN MHI ♦ DIYL YTS

FIG. 42

MKNITFIFFILLASPLYANGDRLYRADSRRPDEIKRFRSLMPRGNEYFDRGT

♥ ALLMOTIS ♥

♥ QMNINLYDHARGTQTGFVRYDDGYV

♦ 107x178x4 ♦

♦ STSLSLRSAAHLAGQYILSGYSLTDIVI ♦ ANMFNVNDVISVY ♥

SP HP YEQEV SAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQA WRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ ALLMOTIS ♥

♥ ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL ♥

FIG. 43

MMFSGFNADY EASSSRCSSA SPAGDSL SYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA

LVSSVAPSQT RAPHFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil
QSIGRRGKVE QLSPEEEKR RIRRE *RNKMA AAK

▲ 107x178x4 ▲

♥ ALLMOTIS ♥

♥ CRNRRRREL ▲ TDTLQAETDQLEDEKSALQTEIANLLKEKEKL ♥

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAF TPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

FIG. 44

SGWESYYKTEGDEEAEEEQEEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCISVYISKIISDRDLLAVVFYGTEKDKN
VNFKNIYVLQELDNPAGAKRILELDQFKGQQGQKRFQDMMGHGS
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

▲107x178x4▲

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

♥LRVH *FEE ♠SSKLEDLLRKVRAKETRKRALSRKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♣ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE
ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK
IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIIVEKLRFTYRS
DSFENPVLQQHFRNLEALALDLME

♦P12LZIPC♦

♦PEQAVDLTLPKVEAMNKRL♦ GSLVDEFKELVYPPDYNPEGKVTKR
KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMILKEACRAYGLKSG
LKKQELLEALTKHFQD

FIG. 45

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♦107x178x4♦

♥ALLMOTI5♥

♥♦LTAWSRTLVTFKDVFVDFTREEWKLLDT♦ AQQIVYRNV
MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR
DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT
HTGEEPYECKECGKSFSWFSHLVTHQRTHGDKLYTCNQCGKSFVH
SSRLIRHQRTHGTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♦P23LZIPC♦

♦PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♦ RENAY

F I G. 46

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FIG. 47

Simian Immunodeficiency Virus M4251		Antifiral Activity SIV																														
DP178-like	Residue	T	W	Q	A	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	201	Residue	47
	245	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q			
	246	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	200	Residue	35
	247	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	281	Residue	35
	248	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	282	Residue	35
	249	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	283	Residue	35
	250	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	284	Residue	35
	251	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	285	Residue	35
	252	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	286	Residue	35
	253	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	287	Residue	35
	254	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	288	Residue	35
	255	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	289	Residue	35
	256	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	290	Residue	35
	257	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	291	Residue	35
	258	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	292	Residue	35
	259	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	293	Residue	35
	260	T	W	Q	E	R	K	V	D	F	L	E	N	I	T	A	L	E	A	A	Q	E	K	N	M	Y	E	L	Q	294	Residue	35

F16. 48

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EE: 49 A

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F.I. 49 C

FEB. 50

EPSTEIN-BARR VIRUS 6 STRAIN B96-8-B2LF1 TRANSACTIVATOR PROTEIN EB1 OR ZEBRA																																												
Residue	173	9	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	218	ACT	Res.	
T-423	173	9	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	208	++*	36	
T-424	173	9	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	208	-	36	
T-425	174	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	210	-	36	
T-426	176	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	211	-	36	
T-427	177	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	212	-	36	
T-428	178	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	213	-	36	
T-429	-	179	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	214	-	36
T-430	-	180	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	216	-	36
T-431	-	181	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	216	-	36
T-432	-	182	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	217	-	36
T-433	-	183	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	218	-	36
T-434	-	184	-	E	L	E	I	K	R	Y	K	N	V	A	8	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	B	E	N	D	R	L	L	L	219	-	36
Residue	186	A	S	A	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	230	ACT	Res.										
T-435	186	A	S	A	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	220	-	36										
T-436	186	B	A	R	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	221	-	36											
T-437	187	-	A	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	222	-	36												
T-438	188	-	K	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	223	-	36													
T-439	188	-	C	R	A	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	224	++*	36														
T-440	189	-	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	226	-	36														
T-441	191	-	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	228	-	36															
T-442	192	-	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	227	-	36																
T-443	193	-	F	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	228	-	36																	
T-444	194	-	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	229	+	36																		
T-445	195	-	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	230	+	36																		
T-446	196	-	K	Q	L	Q	H	Y	R	E	V	A	A	K	G	S	E	N	D	R	L	L	L	231	-	36																		

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Residue	187	L A H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V O S I I P R T P D V L H E D	242	45
T-447	187	L Q H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	232	36
T-448	188	Q H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	233	36
T-449	189	H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	234	36
T-450	200	Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	235	36
T-461	201	R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	236	36
T-462	202	E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	237	36
T-483	203	V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	238	36
T-484	204	A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	239	36
T-485	205	A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	240	36
T-486	206	A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	241	36
T-487	207	K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	242	36
T-488	208	K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	243	36

Residue	209	S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L N F	Residue	246	37
T-459	209	S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L N F		244	36
T-480	210	E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L N F		245	36
T-481	211	N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L N F		246	36

1-16. 51B

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Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-N-W-T-S-L-N-F-L-G-G-T-T
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

1=16, 52 A

Domain II:

223P-G-Y-R-W-M-C-L-R-R-F-I-H-F-L-FI-L-L-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-J-P-G-S-S-T-S-T-G-P-C-R-T-C-M-T-T291

P-Q-Y-R-W-M-C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-
 G-Y-i-R-W-M-C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P
 Y-R-H-M-C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V
 R-W-M-C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C
 W-M;C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P
 M-C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L
 C-L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I
 L-R-R-F-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P
 R-R;P-R-P-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P
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 P-I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S
 I-I-F-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T
 I-F-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S
 P-L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-O
 L-F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-O
 F-I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-O-P
 I-L-L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C
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 L-J-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T
 I-C-L-J-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C
 C-L-I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C-N
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 I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C-N-T

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